IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s):	Itzhak Bentwich	Art Unit:	1635
App. No.:	10/604,984	Examiner:	VIVLEMORE, TRACY ANN
Conf. No.:	1983	Title:	BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES AND USES THEREOF
Filing Date:	August 29, 2003		

DECLARATION OF AYELET CHAJUT, PH.D.

Dear Sir:

I, Ayelet Chajut, Ph.D., hereby declare as follows:

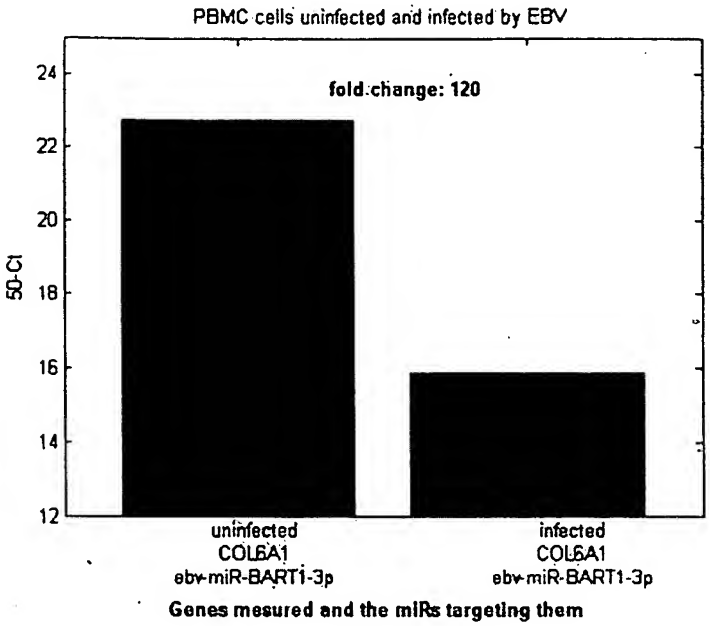
1. I am the Executive Vice President, R&D at Rosetta Genomics, Ltd. ("Rosetta"). A true and correct copy of my Curriculum Vitae is attached to this declaration as Exhibit A.
2. I have 22 years of experience designing and performing experiments in the field of molecular biology, 2.5 of which were related to miRNA biology. I have also worked in the biotechnology industry for 10 years.
3. As a result of my work as Executive Vice President, R&D and experience in the field of molecular biology, I supervised and conducted the two sets of experiments described herein at items 4-7.
4. In order to confirm that nucleic acids related to the ebv-mir-BART1-3P nucleic acid having SEQ ID NO: 4642 affect the levels of the asserted target transcript COL6A1, the methods described in item 5 below were used.
5. The experiments entailed infecting Peripheral Blood Mononuclear Cells (PBMC), which do not express Epstein-Barr virus miRNAs, with Epstein-Barr virus, and then comparing the levels of target COL6A1 mRNA in infected and uninfected cells. RNA was extracted from infected and uninfected PBMC, and COL6A1 mRNA was quantified using the specific primers listed in the table below by the SYBR qRT-PCR method (Applied Biosystems). mRNAs of the housekeeping genes TBP and RPS20 were also quantified by this method using the primers shown in the table below.

Primer_id	Sequence	Gene name
16339-Fwd	GCTGGTCAAGGAGAACTATGC	COL6A1
16340-Rev	TGGTGGTGTCAAAGTTGTGG	COL6A1
16341-Fwd	CAGCTCAATGTCATTTCTTGC	COL6A1
16342-Fwd	CCATGAAATACACGCTGTGC	SNPH
16343-Rev	ACTCCTCCTCAATCCAGTCC	SNPH
16344-Fwd	CAGAAGGAGGTGTGCATCC	SNPH
16345-Rev	GCTTGAGCTGCTTGATCTCC	SNPH

	Primers for Target	
House keeping gene	Fwd	Rev
TBP	TATAATCCCAAGCGGTTTGC	CACAGCTCCCCACCATATTC
RPS20	TATAATCCCAAGCGGTTTGC	CACAGCTCCCCACCATATTC

Total RNA was isolated by EZ-RNA II kit (Biological Industries). 1µg of total RNA was reverse transcribed using Supercript II. After reverse transcription, 10ng of cDNA were used in a qRT-PCR reaction. mRNA was quantified by qRT-PCR SYBR Green method (Applied Biosystems) using 7500 Fast Real Time PCR system. Each test was done in triplicate. Measuring the amount of initial mRNA was based on the observation that the amount of cDNA generated from the mRNA doubles with every cycle of PCR. Therefore, after N cycles, there is 2^N times as much. The initial amount of mRNA was quantified by measuring the cycle number at which the increase in fluorescence (and thus the amount of cDNA) was exponential. A threshold at this level of fluorescence was set. The cycle at this point is indicated as the cycle threshold, or Ct. To compare the differences in quantity between a specific mRNA in two different samples, the 50-Ct value was calculated from the Ct value for each of the samples, and the delta 50-Ct (d50-Ct) was calculated. The fold-change between the amount of mRNA in the two samples was represented by $2^{d50\text{-}Ct}$. The statistical method used to analyze the data was a t-test (two-sided unpaired t-test) between the negative control and the treated samples. Normalization was done by subtracting the Ct values of the housekeeping genes TBP and RPS20. Ct values were determined using a default threshold of 0.2 in the 7500 Fast Real time PCR system (Applied Biosytems), and Ct values were normalized to the housekeeping genes TBP and RPS20.

6. Results of COL6A1 expression in Epstein-Barr virus-infected and uninfected PBMC are shown below:



The above plot shows that the level of COL6A1 mRNA in Epstein Barr virus-infected cells is significantly decreased approximately 120-fold (*i.e.*, $2^{d50\text{-}Ct}=2^{(22.9\text{-}16)}$) as compared to uninfected cells.

7. I solemnly declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like are punishable by fine or imprisonment, or both, under 35 U.S.C. § 1001, and may jeopardize the validity of the application or any patent issuing thereon.

Dated: 29/03/2009 By: _____
Ayelet Chajut, Ph.D.

Exhibit A

CURRICULUM VITAE

AYELET CHAJUT

PERSONAL

Name:	Ayelet Chajut
Date of Birth:	5th August, 1962
Place of Birth:	Israel
Family Status:	Married + 2
Military Service:	1980-1982
Phone:	03-5401981, 052-4287229
e. mail address:	mailto:ayelet_ch@rosettagenomics.com

PROFESSIONAL EXPERIENCE

2007- Executive Vice President R&D, Head Molecular Biology, at Rosetta-Genomics.

2006- 2007 Vice President Therapeutics, at Rosetta-Genomics.
In this capacity, I am responsible for the development of new drugs based on microRNAs.

2005-2006 Director of Science & Technology at Quantomix, Ltd.
In this capacity I am responsible for development of biological applications of the WETSEM technology, mainly in the field of metabolic disorders focusing on the drug development and diagnostic areas, collaborations with academia and pharmaceutical companies.

2003-2005 Vice President Research, at Quark Biotech, Inc.
In this capacity, in addition to my previous tasks, I was responsible to the drug discovery units including: Protein expression and purification, bioassay development. Chemical screening, data analysis, hits selection and validation.

2002-2003 Senior director of Target Discovery and Validation, at Quark Biotech, Inc
In this capacity, in addition to my previous tasks, I was responsible to target gene validation processes in 5 different pathology-related research teams

2000-2002 Director of Target Discovery, at Quark Biotech, Inc
In this capacity I headed the multidisciplinary candidate genes selection committee responsible for nominating and selecting the genes that QBI

should focus research and development efforts on. Responsible for Gene-discovery process units (RNA, cDNA libraries, microarray printing, bioinformatic and data analysis).

1998-2000 Senior scientist, in charge of "Stem Cells" research at Quark Biotech. In this capacity I designed a robust gene discovery program aimed at elucidating the mechanisms of pluripotency of Embryonic & Hematopoietic stem cells and identification of new targets. I was responsible for carrying out these plans by managing the internal research efforts as well as collaborations with several leading researchers in the field.

1989-1994 Laboratory instructor and tutor of 3rd year medical students, Department of Microbiology, Faculty of Medicine, Tel-Aviv University

1993-1999 Managing the "Virology" course in the Open University of Israel, Both from the academic aspect and the administrative aspect.

1997-1998 Project manager, Orit – technological R&D center Ltd, Ariel, Israel.

EDUCATION:

1994-1997 Post Doctoral studies in the Laboratory of Prof. Sara Lavi, Department of Cell Research and Immunology, Faculty of Life Sciences, Tel-Aviv University, Tel-Aviv. Main study: Molecular and biochemical characterization of protein phosphatase 2C (PP2C) in eukaryotic cells; Identification of a putative new cell cycle regulator.

1989-1994 Studies towards Ph.D. degree in the Laboratory of Prof. Abraham Yaniv and Prof. Arnona Gazit in the Department of Human Microbiology, Sackler School of Medicine, Tel-Aviv University, Tel-Aviv. Thesis: "Lymphoproliferative disease virus of turkeys Studies of oncogenetic mechanism".

1988-1989 Studies in the Department of Human Microbiology, Sackler School of Medicine, Tel-Aviv University, Tel-Aviv. M.Sc. degree ***(summa cum laude)***.

1983-1986 Studies in the Faculty of Agriculture, Hebrew University, Jerusalem. B.Sc. degree ***(cum laude)***.

RESEARCH EXPERIENCE

Molecular biology, Protein analysis, Cell culture, in vivo models, Bioinformatics, Microarray design and result analysis,. Bioassay development, HTS screening.

Publications

Articles:

1. Gak, E., Yaniv, A., Chajut, A., Ianconescu, M., Tronick, S.R. and Gazit, A. 1989. *Molecular cloning of an oncogenic replication - competent virus that causes lymphoproliferative disease in turkeys.* J. Virol. 63: 2877 - 2880.

2. Chajut, A., Yaniv, A., Avivi, L., Bar-am, I., Tronick, S.R. and Gazit, A. 1990. *A novel approach for establishing common or random integration loci for retroviral genomes.* Nucleic Acid Res. 15: 4299.

3. Chajut, A., Sarid, R., Gak, E., Yaniv, A., Garry, Tronick, S.R. and Gazit, A. 1992. *The lymphoproliferative disease virus of turkeys is a representative of a distinct class within the retroviridae, evolutionary related to the avian sarcoma- leukemia viruses.* Gene 122: 349 - 354.

4. Sarid, R., Chajut, A., Malkinson, M., Tronick, S.R., Gazit, A. and Yaniv, A. 1994. *Diagnostic test for lymphoproliferative disease virus of turkeys, using the polymerase chain reaction.* Am. J. Vet. Res. 55: 769 - 772.

5. Sarid, R., Chajut, A., Gak, E., Oroszlan, S., Tronick, S.R., Yaniv, A. and Gazit, A. 1994. *Nucleotide sequence and genome organization of a biologically active provirus of the lymphoproliferative disease virus of turkeys.* Virology 204: 648 - 691.

6. Yaniv, A., Sarid, R., Chajut, A., Gak, E., Altstock, R., Tronick, S.R. and Gazit, A. 1995. *The lymphoproliferative disease virus (LPDV) of turkeys.* Isr. J. Veter. Med. 50: 87-95.

7. Chajut, A., Gazit, A. and Yaniv, A. 1996. *The turkey c-rap1A proto-oncogene is expressed via two distinct promoters.* Gene 177: 7-10.

8. Seroussi E, Shani N, Ben-Meir D, Chajut A, Divinski I, Faier S, Gery S, Karby S, Kariv-Inbal Z, Sella O, Smorodinsky NI and Lavi S. 2001. *Uniquely conserved non-translated regions are involved in generation of the two major transcripts of protein phosphatase 2Cbeta.* J Mol Biol. 312:439-51.

9. Shoshani T, Faerman A, Mett I, Zelin E, Tenne T, Gorodin S, Moshel Y, Elbaz S, Budanov A, Chajut A, Kalinski H, Kamer I, Rozen A, Mor O, Keshet E, Leshkowitz D, Einat P, Skaliter R. and Feinstein E. 2002. *Identification of a novel hypoxia-inducible factor 1-responsive gene, RTP801, involved in apoptosis.* Mol Cell Biol. 22:: 2283-93.